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FIGURES

FIG. 1

20 CCACCTTCCCACTTCTCCCAATTCCTTCCTTCCGCTTCGCAAGTCCAA GCCCAAAAGAAAA 50
 20 TCACAAGTCAA GAAGTAAAGAGAGG CACAATTTCATCTATTCTAGGGCTTCTTGGC 120
 ATTTTTCATCCCTTTTAAAGATG GAGTTCCCAATTCAGGAGCTGAGA GCTCTTACCCAAAA 180
 N S E A N O A F E S S T D K
 AAAAAAGGCAAGAGCAAAAGTCAATTAAGG GATTCGAAAGCACTA GCAATTCGAGAGG 240
 K D G R G K I S X K S I S N S I N S V
 CACCTTCTGCAAGCGCCGCAAG GGAATTCCTAAGAGAGGCTATGARTTCTCTGCTCTTGG 300
 T F C R R N N S L L K K A X N L S V L C
 TATGCTGAAGTTCCTCTTATC GTCTTCTGCA GCGGTGGCGCGCTATGAGTATCTAA 360
 T K E V A L I V F S L R S R L E E A H
 CACAGCTCTTCAAGCAACATC GACAGTACAAAAAGCAGTCGCTGATCTTACGAGAGG 420
 N S V R A T I D R T K K A C A D S I E G <-dom:
 GCGATCTGAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAG 480
 D S V S R A W T D F V Q C R A N E F H R
 ACAGATCCGAGCAATTCAGATTCAGACAGGATATATCTCGGCGAATCCCTTACGAGCTT 540
 Q I R E I C N S M R H I D S E L S T L
 GAAAGTCAAGGCACTGAAAGAGCTGAAAGAGGAGTTCAGAGGAGGAGGAGGAGGAGGAG 600
 K V E E L R N L E G R R E E E C I E R I R
 ATCCAAAAAGATGAAATCTCTGTTTCTGAAATCGGATTCATGCAAGAGAGGAGAGCTGA 660
 S K F N E I E F S E I E F N Q N R E F E
 GCTGCAACAGGCAACGATTTCTGAGAGGCAAGAGATAGGCGAAGAGGAGAGAGAGAGGAG 720
 E Q S H N N E D R A K I A E S E R E Q Q
 GAGGAGGAG 780
 Q Q C T K M I P P F S Y D P S K P S K S
 GATGAG 840
 V D P R N F F P V I L E S N N E N Y P R Q
 AGGAG 900
 Q Q I A L O L V
 CAGATCTGAG 960
 GATGAG 1020
 KATTCCTGAG 1085

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FIG. 2

GCAATTCTTCCTTCCCGTTGCCAAGTGCAACCCCAATAGAAAACTCAAAGTCAAGAACT 60
 AGCTAACAGAGAAAAACCACAATTCATCAATTTGGAGGGGTTTTTGCCATTTTTCATCCTT 120
 GCAACAATGGAGTTCCCAATCAAGCACCCGAGAGCTCCTCCAGAAAAAATTGGGAAGG 180
 M E F P N Q A P E S S S Q K K L G R MADS-BOX
 GGCAAAATTGAGATTAGCGGATCGAAAACTACAAATCGACAAGTTACCTTCTGCAA 240
 G K I E I K R I E N T T N R Q V T F C K
 CGCCGCAACGGATTGCTTAAGAAAGCCTATGAATTGCTGTTCTTTGTGATGCTGAAGTT 300
 R R N G L L K K A Y E L S V L C D A E V
 GCTCTTATCGTGTTCCTCAACCGTGCCGCTCTATGAGTATGCTAACAAACAGTGTAGA 360
 A L I V F S N R G R L Y E Y A N N S V R
 GCAACAATCGACAGGTACAAAAAGCATACTGATCCTACGAACAGTGGATCTGTTTCA 420
 A T I D R Y K K A Y A D P T N S G S V S K-domain
 GAAGCCAACACTCAGTTTTATCAGCAGGAAGCATCCAAACTGCGAAGACAGATCCGAGAA 480
 E A N T Q F Y Q Q E A S K L R R Q I R E
 ATTCAGAATTCAAACAGGCATATCTGGGTGAAGCTCTTAGCTCCTTGAACGCCAAGGAA 540
 I Q N S N R H I L G E A L S S L N A K E
 CTGAAGAACCTAGAAGGAAGATTGGAGAAAGGAATCAGCAGAATAAGATCCAAAAAGAA 600
 L K N L E G R L E K G I S R I R S K K N
 GAAATGCTGTTTTCTGAAATCGAATTCATGCAAAAAAGGGAGACCGAGCTGCAACACCAC 660
 E M L F S E I E F M Q K R E T E L Q H H
 AACAAATTTCTGAGAGCAAAGATAGCTGAAAAAGAGAGGGAAGAGCAGCAGCATACACAC 720
 N N F L R A K I A E N E R E E Q Q H T H
 ATGATGCCGGGAACCTCCTACGATCAGTCAATGCCTTCGCATTCTTATGACAGGAACTTC 780
 M M P G T S Y D Q S M P S H S Y D R N F
 CTCCAGCGGTGATCTTGGAGTCCAACAATAACCATTACCTCACCAAGTCCAGACAGCT 840
 L P A V I L E S N N N H Y P H Q V Q T A
 CTCCAACCTGTTTGAATGCTGGACTGCCGTCTGAT 876
 L Q L V .

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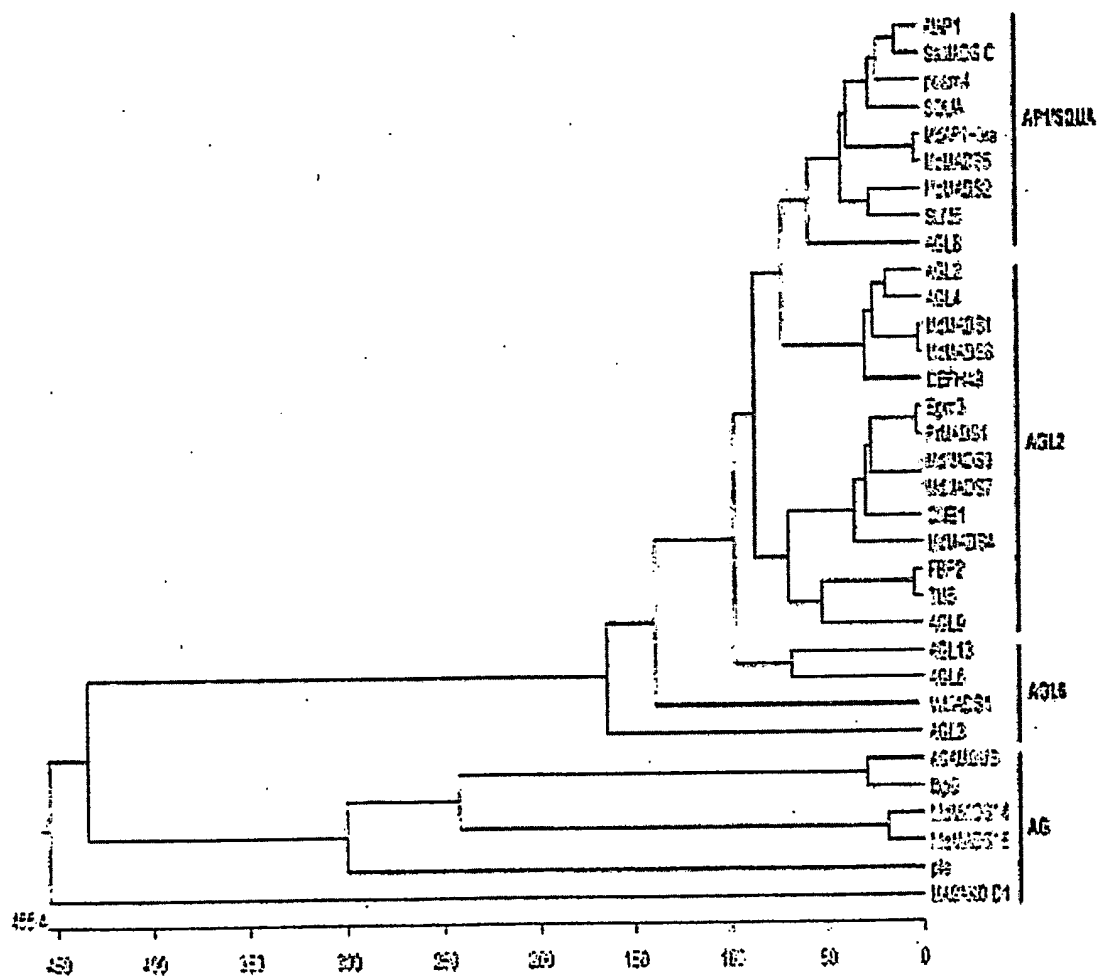
FIG. 3

1	MEFANQAPESST	QKKLGRGKIEIKRIENTT	McMADS14	
1	MEFPNQAPESSS	QKKLGRGKIEIKRIENTT	McMADS16	
31	NRQVTFCKRRNGLLKKAYELSVLCDAEVAL		McMADS14	
31	NRQVTFCKRRNGLLKKAYELSVLCDAEVAL		McMADS16	
61	IVFSTRGRLYEYANNNSVRATIDRYKKA	CAD	McMADS14	
61	IVFSNRGRLYEYANNNSVRATIDRYKKA	YAD	McMADS16	
91	STDGGSVSEANTQFYQQEASKLRRQIREIQ		McMADS14	
91	PTNSGSVSEANTQFYQQEASKLRRQIREIQ		McMADS16	
121	NSNRHILGESLST	LKVKELEKGRLEKGI	McMADS14	
121	NSNRHILGEALSS	LWAKELEKGRLEKGI	McMADS16	
151	SRIRSKKNEILFSEIEFMQKRETELQHHNM		McMADS14	
151	SRIRSKKNEMLFSEIEFMQKRETELQHHNM		McMADS16	
181	FLRAKIAESERE	QQQQTHMIPGTSYD	PSM	McMADS14
181	FLRAKIAEN	EREQQH	-THMMPGTSYDQSM	McMADS16
211	PSNSYDRNFFP	-VILESNNNHYP	RQGQTAL	McMADS14
210	PSHSYDRNFLPA	VILESNNNHYP	HQVQTAL	McMADS16
240	QLV (100%)			McMADS14
240	QLV (88.4%)			McMADS16

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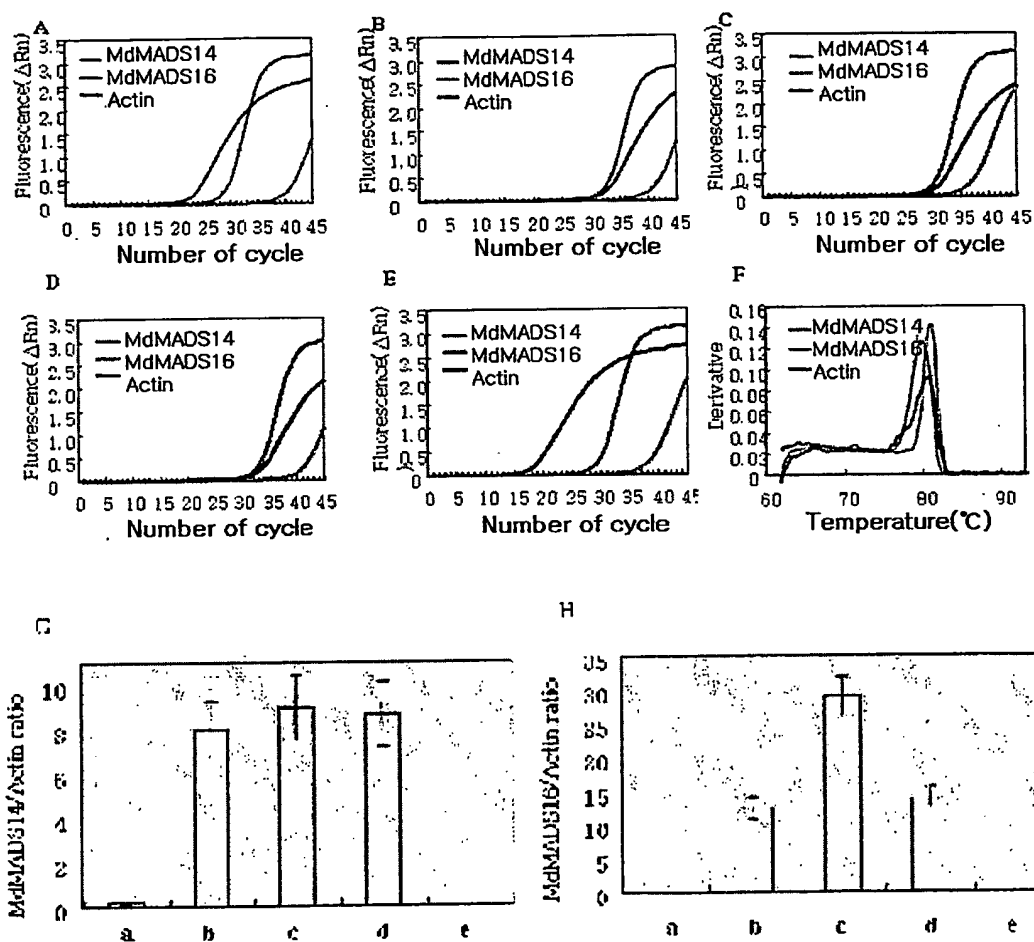
FIG. 4



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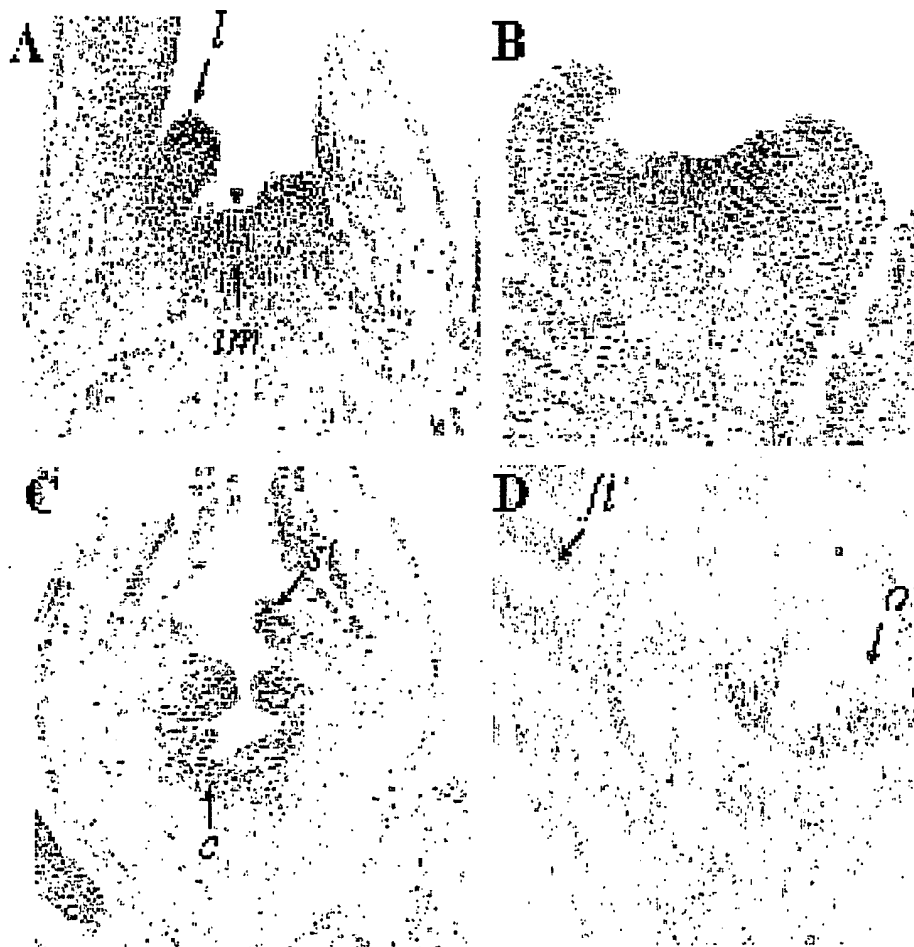
FIG. 5



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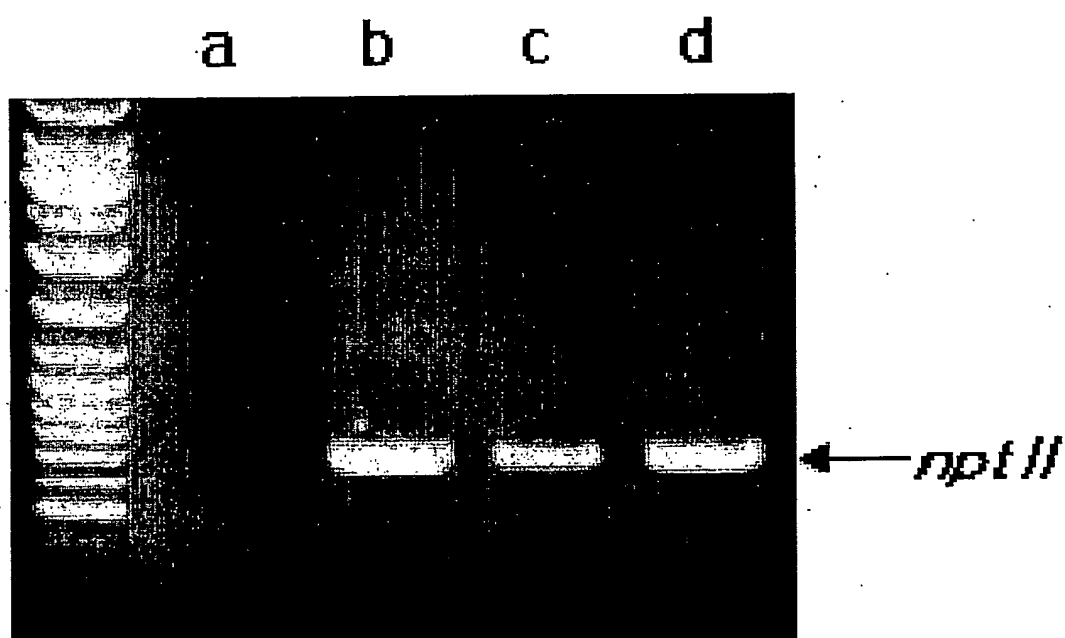
FIG. 6



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FIG. 7



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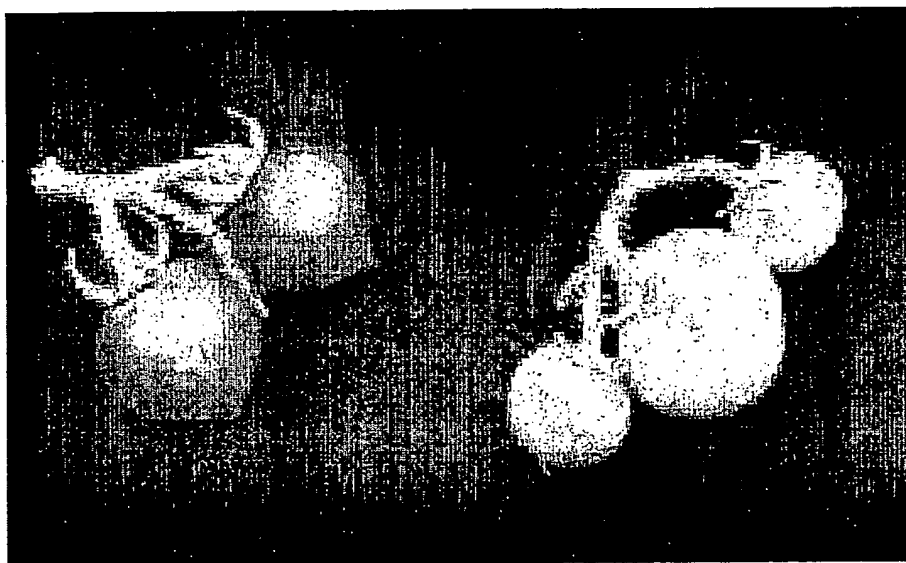
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FIG. 8

Wild type

MdMADS14

Sense 1



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